

# SEQUENCE LISTING

<110> Croteau, Rodney B  
Burke, Charles C

<120> GERANYL DIPHOSPHATE SYNTHASE LARGE SUBUNIT, AND METHODS  
OF USE

<130> WSUR1117920

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<150> 09/420,211

<151> 1999-10-18

<150> PCT/US98/21772

<151> 1998-10-15

<150> 08/951,924

<151> 1997-10-16

<160> 15

&lt;170&gt; PatentIn Ver. 2.0

 $\langle 210 \rangle$  1

<211> 1131

<212> DNA

<213> *Mentha piperita*

<220>

<221> CDS

<222> (1) .. (1131)

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Met Ser Ala Leu Val Asn Pro Val Ala Lys Trp Pro Gln Thr Ile Gly  
1 5 10 15

gtt aaa gat gtt cac ggc ggc cgg agg cgg aga tcc aga tcc act ctc 96  
Val Lys Asp Val His Gly Gly Arg Arg Arg Arg Ser Arg Ser Thr Leu  
20 25 30

ttt caa tcc cat cca ctt cgc act gaa atg cct ttc tct ctc tac ttc 144  
Phe Gln Ser His Pro Leu Arg Thr Glu Met Pro Phe Ser Leu Tyr Phe  
35 40 45

tca tcc ccc ctc aaa gct ccc gcc act ttt tcc gtt tct gca gtt tat 192  
Ser Ser Pro Leu Lys Ala Pro Ala Thr Phe Ser Val Ser Ala Val Tyr  
50 55 60

acc aaa gag ggc agc gaa att agg gat aaa gat ccg gcg cct tcg act 240  
Thr Lys Glu Gly Ser Glu Ile Arg Asp Lys Asp Pro Ala Pro Ser Thr  
65 70 75 80

tcg	ccg	gcg	ttc	gat	ttc	gac	gga	tac	atg	ctc	cgg	aag	gcg	aaa	tcc	288
Ser	Pro	Ala	Phe	Asp	Phe	Asp	Gly	Tyr	Met	Leu	Arg	Lys	Ala	Lys	Ser	
				85					90					95		

gtc aac aag gcg ttg gaa gcg gcg gtg cag atg aag gag ccg ctg aag 336

Val	Asn	Lys	Ala	Leu	Glu	Ala	Ala	Val	Gln	Met	Lys	Glu	Pro	Leu	Lys	
			100				105						110			
atc	cac	gag	tcc	atg	cgg	tac	tcc	ctt	ctc	gcc	ggc	ggc	aag	aga	gtg	384
Ile	His	Glu	Ser	Met	Arg	Tyr	Ser	Leu	Leu	Ala	Gly	Gly	Lys	Arg	Val	
			115				120						125			
cgt	cct	atg	ctg	tgc	atc	gcg	gcc	tgc	gag	ctc	gtc	ggc	ggc	gac	gag	432
Arg	Pro	Met	Leu	Cys	Ile	Ala	Ala	Cys	Glu	Leu	Val	Gly	Gly	Asp	Glu	
			130				135						140			
tcc	acg	gcg	atg	ccg	gcg	gcc	tgc	gcc	gtc	gag	atg	atc	cac	acg	atg	480
Ser	Thr	Ala	Met	Pro	Ala	Ala	Cys	Ala	Val	Glu	Met	Ile	His	Thr	Met	
			145				150						155	160		
tcg	ctg	atg	cac	gac	gac	ctc	cca	tgc	atg	gac	aac	gac	gac	ctc	cgc	528
Ser	Leu	Met	His	Asp	Asp	Leu	Pro	Cys	Met	Asp	Asn	Asp	Asp	Leu	Arg	
			165				170						175			
cgc	ggc	aag	ccg	acg	aac	cac	atg	gct	ttc	ggc	gag	agc	gtg	gcg	gtc	576
Arg	Gly	Lys	Pro	Thr	Asn	His	Met	Ala	Phe	Gly	Glu	Ser	Val	Ala	Val	
			180				185						190			
ctc	gcc	ggc	gac	gcc	ctc	ctc	tcc	ttc	gcg	ttc	gag	cac	gtg	gcg	gcg	624
Leu	Ala	Gly	Asp	Ala	Leu	Leu	Ser	Phe	Ala	Phe	Glu	His	Val	Ala	Ala	
			195				200						205			
gcg	acc	aaa	ggc	gcg	ccg	ccg	gag	cgg	atc	gtg	agg	gtc	ctc	ggc	gag	672
Ala	Thr	Lys	Gly	Ala	Pro	Pro	Glu	Arg	Ile	Val	Arg	Val	Leu	Gly	Glu	
			210				215						220			
ctg	gct	gtc	tcg	atc	ggg	tcg	gag	ggg	ctg	gtg	gcg	ggg	cag	gtg	gtg	720
Leu	Ala	Val	Ser	Ile	Gly	Ser	Glu	Gly	Leu	Val	Ala	Gly	Gln	Val	Val	
			225				230						235	240		
gac	gtc	tgc	tcg	gag	ggg	atg	gcg	gag	gtc	ggg	ctg	gac	cac	ctc	gag	768
Asp	Val	Cys	Ser	Glu	Gly	Met	Ala	Glu	Val	Gly	Leu	Asp	His	Leu	Glu	
			245				250						255			
ttc	atc	cac	cac	cac	aag	acg	gcg	gcg	ctg	ctg	cag	ggg	tcg	gtg	gtt	816
Phe	Ile	His	His	His	Lys	Thr	Ala	Ala	Leu	Leu	Gln	Gly	Ser	Val	Val	
			260				265						270			
ctg	ggg	gcg	att	ttg	ggc	ggc	gga	aag	gag	gag	gag	gtg	gcg	aag	ctg	864
Leu	Gly	Ala	Ile	Leu	Gly	Gly	Gly	Lys	Glu	Glu	Glu	Val	Ala	Lys	Leu	
			275				280						285			
aga	aaa	ttc	gcg	aat	tgc	atc	gga	ttg	ctg	ttt	cag	gtg	gtg	gac	gat	912
Arg	Lys	Phe	Ala	Asn	Cys	Ile	Gly	Leu	Leu	Phe	Gln	Val	Val	Asp	Asp	
			290				295						300			
atc	cta	gat	gtg	acg	aaa	tcg	tcc	aag	gaa	ttg	ggg	aag	acg	gcg	ggg	960
Ile	Leu	Asp	Val	Thr	Lys	Ser	Ser	Lys	Glu	Leu	Gly	Lys	Thr	Ala	Gly	
			305				310						315	320		
aag	gat	ctg	gtg	gcg	gat	aaa	acc	aca	tat	ccg	aag	cta	ata	ggc	gtg	1008
Lys	Asp	Leu	Val	Ala	Asp	Lys	Thr	Thr	Tyr							

340	345	350	
cag ctc ctc cat ttt cat cct cat agg gca gct cca ttg att gct ctc			1104
Gln Leu Leu His Phe His Pro His Arg Ala Ala Pro Leu Ile Ala Leu			
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gcc aat tat att gct tat agg gac aat	1131
Ala Asn Tyr Ile Ala Tyr Arg Asp Asn	
370	375

<210> 2  
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 <213> Mentha piperita

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Met Ser Ala Leu Val Asn Pro Val Ala Lys Trp Pro Gln Thr Ile Gly	
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Val Lys Asp Val His Gly Gly Arg Arg Arg Arg Ser Arg Ser Thr Leu	
20	30
Phe Gln Ser His Pro Leu Arg Thr Glu Met Pro Phe Ser Leu Tyr Phe	
35	45
Ser Ser Pro Leu Lys Ala Pro Ala Thr Phe Ser Val Ser Ala Val Tyr	
50	60
Thr Lys Glu Gly Ser Glu Ile Arg Asp Lys Asp Pro Ala Pro Ser Thr	
65	80
Ser Pro Ala Phe Asp Phe Asp Gly Tyr Met Leu Arg Lys Ala Lys Ser	
85	95
Val Asn Lys Ala Leu Glu Ala Ala Val Gln Met Lys Glu Pro Leu Lys	
100	110
Ile His Glu Ser Met Arg Tyr Ser Leu Leu Ala Gly Gly Lys Arg Val	
115	125
Arg Pro Met Leu Cys Ile Ala Ala Cys Glu Leu Val Gly Gly Asp Glu	
130	140
Ser Thr Ala Met Pro Ala Ala Cys Ala Val Glu Met Ile His Thr Met	
145	160
Ser Leu Met His Asp Asp Leu Pro Cys Met Asp Asn Asp Asp Leu Arg	
165	175
Arg Gly Lys Pro Thr Asn His Met Ala Phe Gly Glu Ser Val Ala Val	
180	190
Leu Ala Gly Asp Ala Leu Leu Ser Phe Ala Phe Glu His Val Ala Ala	
195	205
Ala Thr Lys Gly Ala Pro Pro Glu Arg Ile Val Arg Val Leu Gly Glu	
210	220
Leu Ala Val Ser Ile Gly Ser Glu Gly Leu Val Ala Gly Gln Val Val	
225	240

TCF80B24E66

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<212> PRT  
<213> Mentha piperita

<400> 6  
Glu Ala Val Glu Thr Leu Leu His Phe  
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<212> DNA  
<213> Artificial Sequence

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<223> Description of Artificial Sequence:  
oligonucleotide

<220>  
<221> misc\_feature  
<222> (1)..(26)  
<223> PCR primer GG23F

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gaattgcatac ggattgctgt ttcagg 26

<210> 8  
<211> 24  
<212> DNA  
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oligonucleotide

<220>  
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<210> 9  
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ccaaggaatt ggggaagacg gcggggaagg atctggtggc g 101

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ctc aaa aca aga tct gat ctc agc cgt tct tct tcc gcg cgt tgc atg 98  
Leu Lys Thr Arg Ser Asp Leu Ser Arg Ser Ser Ser Ala Arg Cys Met  
20 25 30

cca act gcc gcc gct gcc gcc ttc ccc act atc gcc acc gcc gcc caa 146  
Pro Thr Ala Ala Ala Ala Ala Phe Pro Thr Ile Ala Thr Ala Ala Gln  
35 40 45

agt cag ccg tac tgg gcc gcc atc gag gcc gac ata gag aga tac ctg 194  
 Ser Gln Pro Tyr Trp Ala Ala Ile Glu Ala Asp Ile Glu Arg Tyr Leu  
 50 55 60

aag aaa tcc atc aca ata agg ccg ccg gag aca gtt ttc ggg ccc atg 242  
Lys Lys Ser Ile Thr Ile Arg Pro Pro Glu Thr Val Phe Gly Pro Met  
65 70 75

cac cac ctc acc ttc gcc gcc cca gcc acc gcc gcc tcc acc cta tgc 290  
His His Leu Thr Phe Ala Ala Pro Ala Thr Ala Ala Ser Thr Leu Cys  
80 85 90 95

ttg gcg gcg tgc gag ctc gtc ggc ggc gac cga agc caa gcc atg gca 338  
Leu Ala Ala Cys Glu Leu Val Gly Gly Asp Arg Ser Gln Ala Met Ala  
100 105 110

gcc gcg gcg gcg atc cat ctc gtg cac gcg gca gcc tac gtc cac gag 386  
Ala Ala Ala Ala Ile His Leu Val His Ala Ala Ala Tyr Val His Glu  
115 120 125

cac ctc cct cta acc gac ggg tcg agg ccc gta tcc aag ccc gca atc 434  
 His Leu Pro Leu Thr Asp Gly Ser Arg Pro Val Ser Lys Pro Ala Ile  
 130 135 140

cag cac aag tac ggc ccg aac gtc gag ctc ctc acc gga gac ggg att 482  
Gln His Lys Tyr Gly Pro Asn Val Glu Leu Leu Thr Gly Asp Gly Ile  
145 150 155

gtc ccg ttc ggg ttt gag ttg ctg gcc ggg tca gtg gac ccg gcc cga 530  
Val Pro Phe Gly Phe Glu Leu Leu Ala Gly Ser Val Asp Pro Ala Arg  
160 165 170 175

aca gac gac ccg gat agg att ctg aga gtt ata ata gag atc agt cgg 578  
Thr Asp Asp Pro Asp Arg Ile Leu Arg Val Ile Ile Glu Ile Ser Arg  
180 185 190

gcc ggc ggg ccg gag gga atg ata agc ggg ctg cat agg gaa gaa gaa 626  
Ala Gly Gly Pro Glu Gly Met Ile Ser Gly Leu His Arg Glu Glu Glu  
195 200 205

att gtt gat gga aat acg agt tta gac ttc att gaa tat gtg tgc aag 674  
Ile Val Asp Gly Asn Thr Ser Leu Asp Phe Ile Glu Tyr Val Cys Lys  
210 215 220

aaa aaa tac ggc gag atg cat gct tgc ggc gcg gct tgt gga gcc ata 722

Lys Lys Tyr Gly Glu Met His Ala Cys Gly Ala Ala Cys Gly Ala Ile  
 225 230 235

ttg ggc ggc gca gcc gag gag gag att cag aag ctg agg aat ttc ggg 770  
 Leu Gly Gly Ala Ala Glu Glu Glu Ile Gln Lys Leu Arg Asn Phe Gly  
 240 245 250 255

ctt tat caa gga act ctc aga gga atg atg gaa atg aaa aat tct cat 818  
 Leu Tyr Gln Gly Thr Leu Arg Gly Met Met Glu Met Lys Asn Ser His  
 260 265 270

caa tta att gat gag aat ata att gga aaa ttg aaa gaa ttg gct ctc 866  
 Gln Leu Ile Asp Glu Asn Ile Ile Gly Lys Leu Lys Glu Leu Ala Leu  
 275 280 285

gag gag ttg gga ggc ttc cac ggg aag aac gct gag ctg atg tcg agc 914  
 Glu Glu Leu Gly Gly Phe His Gly Lys Asn Ala Glu Leu Met Ser Ser  
 290 295 300

ctt gta gcc gag ccg agc ctt tac gcg gct tagagctatt cggatccttc 964  
 Leu Val Ala Glu Pro Ser Leu Tyr Ala Ala  
 305 310

attgcatttt catgcgacat cttcatattc atattgcata atatttttta agccagttat 1024

ttttttatta tgaatttttt taactgttat tgatttcgaa aatactgaca atcatctaaa 1084

ataaagtaaa tataagtaagg atgaaaaaaaa aaaaaaaaaa aaaaaaa 1131

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 <213> Mentha piperita

<400> 11  
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 20 25 30

Thr Ala Ala Ala Ala Ala Phe Pro Thr Ile Ala Thr Ala Ala Gln Ser  
 35 40 45

Gln Pro Tyr Trp Ala Ala Ile Glu Ala Asp Ile Glu Arg Tyr Leu Lys  
 50 55 60

Lys Ser Ile Thr Ile Arg Pro Pro Glu Thr Val Phe Gly Pro Met His  
 65 70 75 80

His Leu Thr Phe Ala Ala Pro Ala Thr Ala Ala Ser Thr Leu Cys Leu  
 85 90 95

Ala Ala Cys Glu Leu Val Gly Gly Asp Arg Ser Gln Ala Met Ala Ala  
 100 105 110

Ala Ala Ala Ile His Leu Val His Ala Ala Ala Tyr Val His Glu His  
 115 120 125

Leu Pro Leu Thr Asp Gly Ser Arg Pro Val Ser Lys Pro Ala Ile Gln

107283 = 824466

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His Lys Tyr Gly Pro Asn Val Glu Leu Leu Thr Gly Asp Gly Ile Val		
145	150	155
Pro Phe Gly Phe Glu Leu Leu Ala Gly Ser Val Asp Pro Ala Arg Thr		
	165	170
Asp Asp Pro Asp Arg Ile Leu Arg Val Ile Ile Glu Ile Ser Arg Ala		
	180	185
Gly Gly Pro Glu Gly Met Ile Ser Gly Leu His Arg Glu Glu Glu Ile		
	195	200
Val Asp Gly Asn Thr Ser Leu Asp Phe Ile Glu Tyr Val Cys Lys Lys		
	210	215
Lys Tyr Gly Glu Met His Ala Cys Gly Ala Ala Cys Gly Ala Ile Leu		
	225	230
Gly Gly Ala Ala Glu Glu Glu Ile Gln Lys Leu Arg Asn Phe Gly Leu		
	245	250
Tyr Gln Gly Thr Leu Arg Gly Met Met Glu Met Lys Asn Ser His Gln		
	260	265
Leu Ile Asp Glu Asn Ile Ile Gly Lys Leu Lys Glu Leu Ala Leu Glu		
	275	280
Glu Leu Gly Gly Phe His Gly Lys Asn Ala Glu Leu Met Ser Ser Leu		
	290	295
Val Ala Glu Pro Ser Leu Tyr Ala Ala		
	305	310

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<210> 13  
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<400> 13  
 Val Ile Ile Glu Ile Ser  
 1 5

<210> 14  
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<223> Description of Artificial Sequence:  
oligonucleotide

<221> misc feature

<223> Forward PCR primer for cloning geranyl diphosphate

<400> 14

18

<211> 17

<213> Artificial Sequence

<223> Description of Artificial Sequence:  
oligonucleotide

<221> misc feature

<223> Reverse PCR primer for cloning geranyl diphosphate

<400> 15

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